



PCT09

ENTERED

RAW SEQUENCE LISTING

DATE: 03/19/2003

PATENT APPLICATION: US/09/701,271A

TIME: 14:23:40

Input Set : A:\Seqlist.txt

Output Set: N:\CRF4\03192003\I701271A.raw

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4 <110> APPLICANT: Ruelle, Jean-Louis
5      Tommassen, Johannes Petrus Maria
7 <120> TITLE OF INVENTION: Neisseria Meningitidis Antigenic
8      Polypeptides, Corresponding Polynucleotides and Protective
9      Antibodies
11 <130> FILE REFERENCE: BM45323
13 <140> CURRENT APPLICATION NUMBER: 09/701,271A
14 <141> CURRENT FILING DATE: 2000-11-27
16 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03603
17 <151> PRIOR FILING DATE: 1999-05-26
19 <150> PRIOR APPLICATION NUMBER: 9811260.0
20 <151> PRIOR FILING DATE: 1998-05-26
22 <160> NUMBER OF SEQ ID NOS: 8
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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28 <212> TYPE: DNA
29 <213> ORGANISM: Neisseria meningitidis
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34 atcgtcaaag tcagctttga caaagagatt gtcaaccgca ccggcttcgt aacctcctca      180
35 ccggcccgcga tcgccttggc ctttgaacaa accggcattt ccatggatca acaggtactc      240
36 gaatatgccg atcctctgtt gagcaaaatc agtgccgcac aaaacagcag ccgtgcgcgt      300
37 ctggtttctga atctgaacaa accgggcca aacaataaccg aagtacgcgg gaacaaagt      360
38 tggatattca ttaacgaatc ggacgatacc gtgtccgccc ccgcacgccc cgccgtaaaa      420
39 gccgcgcctg ccgcaccggc aaaacaacag ggctgccgca ccgtctacca agtccgcagt      480
40 atccgtatcc aaacccttta ccccggaaca acaacagctg ccgcaccgtt taccgagtcc      540
41 gtagtatccg tatccgcacc gttagcggcg gcaaaacaac aggcggcgcc atcagcaaaa      600
42 caacagacgg cagcaccagc aaaacaacag acggcagcac cagcaaaaca acaggcggca      660
43 gcaccagcaa aacaaacca tatcgatttc cgcaaagacg gcaaaaatgc cggcattatc      720
44 gaattggctg cattgggctt tgccggggcag cccgacatca gccaacagca cgaccacatc      780
45 atcgttacgc tgaaaaacca taccctgccg accacgctcc aacgcagttt ggatgtggca      840
46 gactttaaaa caccggttca aaaggttacg ctgaaacgcc tcaataacga caccagctg      900
47 attatcacia cagccggcaa ctgggaactc gtcaacaaat ccgccgcgcc cggatacttt      960
48 accttccaag tcttgccgaa aaaacaaaac ctcgagtcag gcggcgtgaa caatgcgccc      1020
49 aaaaccttca caggccggaa aatctccctt gacttccaag atgtcgaaat ccgcaccatc      1080
50 ctgcagattt tggcaaaaga atccgggatg aacattgttg ccagcgactc cgtcaacggc      1140
51 aaaatgacct tctccctcaa agacgtacct tgggatcagg ctttgattt ggttatgcag      1200
52 gcacgcaacc tcgatatgcg ccaacaaggg aacatcgcca acatcgcgcc ccgcgacgag      1260
53 ctgcttgcca aagacaaagc cttcttacag gcggaaaaag acattgccga tctaggcgcg      1320
54 ctgtattcac aaaacttcca attgaaatac aaaaatgtgg aagaattccg cagcatcctg      1380
55 cgtttggaac atgccgacac aaccggaaac cgcaatacgc ttgtcagcgg caggggcagc      1440

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56 gtgctgatcg atcccgccac caataccctg attgttaccg ataccgcgag cgtcatcgaa 1500
57 aaattccgca aactgattga cgaattggac gtaccgcgcg aacaagtgat gattgaggcg 1560
58 cgtatcgtcg aagcggcaga cggcttctcg cgcgatttgg gcgttaaatt cggcgcgaca 1620
59 ggcaagaaaa agctgaaaaa tgatacaagc gcattcggct ggggggtaaa ctccggcttc 1680
60 ggcggcgacg ataaatgggg ggccgaaacc aaaatcaacc tgccgattac cgctgccgca 1740
61 aacagcattt cgctggtgcg cgcgatttcc tccggtgcct tgaatttgga attgtccgca 1800
62 tccgaatcgc tttaaaaaac caaaacgctt gccaatccgc gcgtgctgac ccaaaaccgc 1860
63 aaagaggcca aaatcgaatc cggttacgaa attcctttca ccgtaacctc aatcgcgaac 1920
64 ggcggcagca gcacgaacac ggaactcaaa aaagccgtct tggggctgac cgttacgccg 1980
65 aacatcacgc ccgacggcca aatcattatg accgtcaaaa tcaacaagga ctgcctgcg 2040
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67 gctatggttg aaaacggcgg cacattgatt gtcggcggtg tttatgaaga agacaacggc 2160
68 aatacgcctg ccaaagtcct cctgttgggc gacatcccg ttatcgcaa cctctttaa 2220
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72 <210> SEQ ID NO: 2

73 <211> LENGTH: 769

74 <212> TYPE: PRT

75 <213> ORGANISM: Neisseria meningitidis

77 <400> SEQUENCE: 2

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81 20 25 30
82 Ser Ser Leu Pro Asn Lys Gln Lys Ile Val Lys Val Ser Phe Asp Lys
83 35 40 45
84 Glu Ile Val Asn Pro Thr Gly Phe Val Thr Ser Ser Pro Ala Arg Ile
85 50 55 60
86 Ala Leu Asp Phe Glu Gln Thr Gly Ile Ser Met Asp Gln Gln Val Leu
87 65 70 75 80
88 Glu Tyr Ala Asp Pro Leu Leu Ser Lys Ile Ser Ala Ala Gln Asn Ser
89 85 90 95
90 Ser Arg Ala Arg Leu Val Leu Asn Leu Asn Lys Pro Gly Gln Tyr Asn
91 100 105 110
92 Thr Glu Val Arg Gly Asn Lys Val Trp Ile Phe Ile Asn Glu Ser Asp
93 115 120 125
94 Asp Thr Val Ser Ala Pro Ala Arg Pro Ala Val Lys Ala Ala Pro Ala
95 130 135 140
96 Ala Pro Ala Lys Gln Gln Gly Cys Arg Thr Val Tyr Gln Val Arg Ser
97 145 150 155 160
98 Ile Arg Ile Gln Thr Leu Tyr Pro Gly Lys Thr Thr Ala Ala Ala Pro
99 165 170 175
100 Phe Thr Glu Ser Val Val Ser Val Ser Ala Pro Phe Ser Pro Ala Lys
101 180 185 190
102 Gln Gln Ala Ala Ala Ser Ala Lys Gln Gln Thr Ala Ala Pro Ala Lys
103 195 200 205
104 Gln Gln Thr Ala Ala Pro Ala Lys Gln Gln Ala Ala Ala Pro Ala Lys
105 210 215 220
106 Gln Thr Asn Ile Asp Phe Arg Lys Asp Gly Lys Asn Ala Gly Ile Ile

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107 225          230          235          240
108 Glu Leu Ala Ala Leu Gly Phe Ala Gly Gln Pro Asp Ile Ser Gln Gln
109          245          250          255
110 His Asp His Ile Ile Val Thr Leu Lys Asn His Thr Leu Pro Thr Thr
111          260          265          270
112 Leu Gln Arg Ser Leu Asp Val Ala Asp Phe Lys Thr Pro Val Gln Lys
113          275          280          285
114 Val Thr Leu Lys Arg Leu Asn Asn Asp Thr Gln Leu Ile Ile Thr Thr
115          290          295          300
116 Ala Gly Asn Trp Glu Leu Val Asn Lys Ser Ala Ala Pro Gly Tyr Phe
117 305          310          315          320
118 Thr Phe Gln Val Leu Pro Lys Lys Gln Asn Leu Glu Ser Gly Gly Val
119          325          330          335
120 Asn Asn Ala Pro Lys Thr Phe Thr Gly Arg Lys Ile Ser Leu Asp Phe
121          340          345          350
122 Gln Asp Val Glu Ile Arg Thr Ile Leu Gln Ile Leu Ala Lys Glu Ser
123          355          360          365
124 Gly Met Asn Ile Val Ala Ser Asp Ser Val Asn Gly Lys Met Thr Leu
125          370          375          380
126 Ser Leu Lys Asp Val Pro Trp Asp Gln Ala Leu Asp Leu Val Met Gln
127 385          390          395          400
128 Ala Arg Asn Leu Asp Met Arg Gln Gln Gly Asn Ile Val Asn Ile Ala
129          405          410          415
130 Pro Arg Asp Glu Leu Leu Ala Lys Asp Lys Ala Phe Leu Gln Ala Glu
131          420          425          430
132 Lys Asp Ile Ala Asp Leu Gly Ala Leu Tyr Ser Gln Asn Phe Gln Leu
133          435          440          445
134 Lys Tyr Lys Asn Val Glu Glu Phe Arg Ser Ile Leu Arg Leu Asp Asn
135          450          455          460
136 Ala Asp Thr Thr Gly Asn Arg Asn Thr Leu Val Ser Gly Arg Gly Ser
137 465          470          475          480
138 Val Leu Ile Asp Pro Ala Thr Asn Thr Leu Ile Val Thr Asp Thr Arg
139          485          490          495
140 Ser Val Ile Glu Lys Phe Arg Lys Leu Ile Asp Glu Leu Asp Val Pro
141          500          505          510
142 Ala Gln Gln Val Met Ile Glu Ala Arg Ile Val Glu Ala Ala Asp Gly
143          515          520          525
144 Phe Ser Arg Asp Leu Gly Val Lys Phe Gly Ala Thr Gly Lys Lys Lys
145          530          535          540
146 Leu Lys Asn Asp Thr Ser Ala Phe Gly Trp Gly Val Asn Ser Gly Phe
147 545          550          555          560
148 Gly Gly Asp Asp Lys Trp Gly Ala Glu Thr Lys Ile Asn Leu Pro Ile
149          565          570          575
150 Thr Ala Ala Ala Asn Ser Ile Ser Leu Val Arg Ala Ile Ser Ser Gly
151          580          585          590
152 Ala Leu Asn Leu Glu Leu Ser Ala Ser Glu Ser Leu Ser Lys Thr Lys
153          595          600          605
154 Thr Leu Ala Asn Pro Arg Val Leu Thr Gln Asn Arg Lys Glu Ala Lys
155          610          615          620

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158 Gly Gly Ser Ser Thr Asn Thr Glu Leu Lys Lys Ala Val Leu Gly Leu
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160 Thr Val Thr Pro Asn Ile Thr Pro Asp Gly Gln Ile Ile Met Thr Val
161                      660                      665                      670
162 Lys Ile Asn Lys Asp Ser Pro Ala Gln Cys Ala Ser Gly Asn Gln Thr
163                      675                      680                      685
164 Ile Leu Cys Ile Ser Thr Lys Asn Leu Asn Thr Gln Ala Met Val Glu
165                      690                      695                      700
166 Asn Gly Gly Thr Leu Ile Val Gly Gly Ile Tyr Glu Glu Asp Asn Gly
167 705                      710                      715                      720
168 Asn Thr Leu Thr Lys Val Pro Leu Leu Gly Asp Ile Pro Val Ile Gly
169                      725                      730                      735
170 Asn Leu Phe Lys Thr Arg Gly Lys Lys Thr Asp Arg Arg Glu Leu Leu
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173                      755                      760                      765
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178 <211> LENGTH: 2310
179 <212> TYPE: DNA
180 <213> ORGANISM: Neisseria meningitidis
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185 atcgtcaaag tcagctttga caaagagatt gtcaaccgca ccggcttcgt aacctcctca      180
186 cgggcccgca tcgccttgga ctttgaacaa accggcattt ccatggatca acaggtaactc      240
187 gaatatgccc atoctctggt gagcaaaatc agtgccgcac aaaacagcag ccgtgcgcgt      300
188 ctggttctga atctgaacaa accgggccaa tacaataccg aagtacgcgg gaacaaagtt      360
189 tggatattca ttaacgaatc ggacgatacc gtgtccgccc ccgcacgccc cgccgtaaaa      420
190 gccgcgcctg ccgcaccggc aaaacaacag gctgccgcac cgtctaccaa gtccgcagta      480
191 tccgtatcca aaccttttac cccggcaaaa caacaggctg ccgcaccgtt taccgagtcc      540
192 gtagtatccg tatccgcacc gttcagcccg gcaaaacaac aggcggcggc atcagcaaaa      600
193 caacagacgg cagcaccagc aaaacaacag acggcagcac cagcaaaaca acaggcggca      660
194 gcaccagcaa aacaaaccaa tatcgatttc cgcaaagacg gcaaaaatgc cggcattatc      720
195 gaattggctg cattgggctt tgccgggcag cccgacatca gccaacagca cgaccacatc      780
196 atcgttacgc tgaaaaacca taccctgccc accacgctcc aacgcagttt ggatgtggca      840
197 gactttaaaa caccggttca aaaggttacg ctgaaacgcc tcaataacga caccagctg      900
198 attatcacia cagccggcaa ctgggaactc gtcaacaaat ccgccgcgcc cggatacttt      960
199 accttccaag tctgcccga aaaacaaaac ctcgagtcag gcggcgtgaa caatgcgccc      1020
200 aaaaccttca caggccggaa aatctccctt gacttccaag atgtcgaaat ccgcaccatc      1080
201 ctgcagattt tggcaaaaga atccgggatg aacattgttg ccagcgactc cgtcaacggc      1140
202 aaaatgaccc tctccctcaa agacgtacct tgggatcagg ctttggattt ggttatgcag      1200
203 gcacgcaacc tcgatacgc ccaacaaggg aacatcgtag acatcgcgcc ccgcgacgag      1260
204 ctgcttgcca aagacaaagc cttcttacag gcggaaaaag acattgccga tctaggcgcg      1320
205 ctgtattcac aaaacttcca attgaaatac aaaaatgtgg aagaattccg cagcatcctg      1380
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210 ggcaagaaaa agctgaaaaa tgatacaagc gcattcggct ggggggtaaa ctccggcttc 1680
211 ggcggcgacg ataaatgggg ggcggaaacc aaaatcaacc tgccgattac cgctgccgca 1740
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223 <210> SEQ ID NO: 4
224 <211> LENGTH: 769
225 <212> TYPE: PRT
226 <213> ORGANISM: Neisseria meningitidis
228 <400> SEQUENCE: 4
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233 Ser Ser Leu Pro Asn Lys Gln Lys Ile Val Lys Val Ser Phe Asp Lys
234 35 40 45
235 Glu Ile Val Asn Pro Thr Gly Phe Val Thr Ser Ser Pro Ala Arg Ile
236 50 55 60
237 Ala Leu Asp Phe Glu Gln Thr Gly Ile Ser Met Asp Gln Gln Val Leu
238 65 70 75 80
239 Glu Tyr Ala Asp Pro Leu Leu Ser Lys Ile Ser Ala Ala Gln Asn Ser
240 85 90 95
241 Ser Arg Ala Arg Leu Val Leu Asn Leu Asn Lys Pro Gly Gln Tyr Asn
242 100 105 110
243 Thr Glu Val Arg Gly Asn Lys Val Trp Ile Phe Ile Asn Glu Ser Asp
244 115 120 125
245 Asp Thr Val Ser Ala Pro Ala Arg Pro Ala Val Lys Ala Ala Pro Ala
246 130 135 140
247 Ala Pro Ala Lys Gln Gln Ala Ala Pro Ser Thr Lys Ser Ala Val
248 145 150 155 160
249 Ser Val Ser Lys Pro Phe Thr Pro Ala Lys Gln Gln Ala Ala Ala Pro
250 165 170 175
251 Phe Thr Glu Ser Val Val Ser Val Ser Ala Pro Phe Ser Pro Ala Lys
252 180 185 190
253 Gln Gln Ala Ala Ala Ser Ala Lys Gln Gln Thr Ala Ala Pro Ala Lys
254 195 200 205
255 Gln Gln Thr Ala Ala Pro Ala Lys Gln Gln Ala Ala Ala Pro Ala Lys
256 210 215 220
257 Gln Thr Asn Ile Asp Phe Arg Lys Asp Gly Lys Asn Ala Gly Ile Ile
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VERIFICATION SUMMARY

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